

M-104

The role of microRNA 319 during soybean (*Glycine max*) nodulation

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It is now well documented that miRNAs play an important role in legume nodulation. Therefore, miRNAs represent another layer of complexity acting either positively or negatively to regulate nodule formation. In a previous publication in which we sequenced a variety of miRNAs from soybean nodule cells, we showed that the relative levels of miRNA 319 were significantly reduced during nodule formation, while the potential targets of this miRNA were expressed significantly higher when measured at five different stages of soybean nodule development. MicroRNA319 has three copies in the soybean genome; namely, miRNA319d, miRNA319i and miRNA319o. These miRNAs have an identical sequence, while their precursor gene sequences show more than 80% similarity. The putative target genes of miRNA 319 were identified by degradome analysis. These targets include the TCP4 (*Teosinte branched 1, Cycloidea, PCF*) and MYB (*myeloblastosis*) transcription factors (TFs). Ectopic over-expression of two independent precursors of microRNA319i and miRNA319o significantly increased nodule numbers on soybean roots when inoculated with *B. japonicum*, suggesting that miR319 positively regulates soybean nodulation, likely by targeting these transcription factors, which presumably act to suppress nodule numbers. Currently, we are targeting three potential target genes of miRNA319 using both RNAi and CRISPR-Cas9 gene editing. Our future work will seek to fully explore more the role of miR319 in the soybean nodulation process.